



## RAW SEQUENCE LISTING ERROR REPORT

The Biotechnology Systems Branch of the Scientific and Technical Information Center (STIC) detected errors when processing the following computer readable form:

Application Serial Number: 10/714,781  
Source: FWO  
Date Processed by STIC: 10-18-04

THE ATTACHED PRINTOUT EXPLAINS DETECTED ERRORS.

PLEASE FORWARD THIS INFORMATION TO THE APPLICANT BY EITHER:

- 1) INCLUDING A COPY OF THIS PRINTOUT IN YOUR NEXT COMMUNICATION TO THE APPLICANT, WITH A NOTICE TO COMPLY or,
- 2) TELEPHONING APPLICANT AND FAXING A COPY OF THIS PRINTOUT, WITH A NOTICE TO COMPLY

FOR CRF SUBMISSION AND PATENTIN SOFTWARE QUESTIONS, PLEASE CONTACT MARK SPENCER, TELEPHONE: 571-272-2510; FAX: 571-273-0221

TO REDUCE ERRORED SEQUENCE LISTINGS, PLEASE USE THE CHECKER  
VERSION 4.2 PROGRAM, ACCESSIBLE THROUGH THE U.S. PATENT AND  
TRADEMARK OFFICE WEBSITE. SEE BELOW FOR ADDRESS

<http://www.uspto.gov/web/offices/pac/checker/chkrnote.htm>

Applicants submitting genetic sequence information electronically on diskette or CD-Rom should be aware that there is a possibility that the disk/CD-Rom may have been affected by treatment given to all incoming mail. Please consider using alternate methods of submission for the disk/CD-Rom or replacement disk/CD-Rom. Any reply including a sequence listing in electronic form should NOT be sent to the 20231 zip code address for the United States Patent and Trademark Office, and instead should be sent via the following to the indicated addresses:

1. EFS-Bio (<<http://www.uspto.gov/ebc/efs/downloads/documents.htm>> , EFS Submission User Manual - cPAVE)
2. U.S. Postal Service: Commissioner for Patents, P.O. Box 1450, Alexandria, VA 22313-1450
3. Hand Carry, Federal Express, United Parcel Service, or other delivery service (EFFECTIVE 06/05/04):  
U.S. Patent and Trademark Office, 220-20<sup>th</sup> Street S., Customer Window, Mail Stop Sequence, Crystal Plaza Two, Lobby,  
Room 1B03, Arlington, VA 22202

Revised 05/17/04

# Raw Sequence Listing Error Summary

## ERROR DETECTED

## SUGGESTED CORRECTION

SERIAL NUMBER: 10/714781

ATTN: NEW RULES CASES: PLEASE DISREGARD ENGLISH "ALPHA" HEADERS, WHICH WERE INSERTED BY PTO SOFTWARE

- 1      Wrapped Nucleics    The number/text at the end of each line "wrapped" down to the next line. This may occur if your file was retrieved in a word processor after creating it. Please adjust your right margin to .3; this will prevent "wrapping."
- 2      Invalid Line Length    The rules require that a line not exceed 72 characters in length. This includes white spaces.
- 3      Misaligned Amino    The numbering under each 5<sup>th</sup> amino acid is misaligned. Do not use tab codes between numbers; use space characters, instead.
- 4      Non-ASCII    The submitted file was not saved in ASCII(DOS) text, as required by the Sequence Rules. Please ensure your subsequent submission is saved in ASCII text.
- 5      Variable Length    Sequence(s)            contain n's or Xaa's representing more than one residue. Per Sequence Rules, each n or Xaa can only represent a single residue. Please present the maximum number of each residue having variable length and indicate in the <220>-<223> section that some may be missing
- 6      PatentIn 2.0    A "bug" in PatentIn version 2.0 has caused the <220>-<223> section to be missing from amino acid sequences(s)           . Normally, PatentIn would automatically generate this section from the previously coded nucleic acid sequence. Please manually copy the relevant <220>-<223> section to the subsequent amino acid sequence. This applies to the mandatory <220>-<223> sections for Artificial or Unknown sequences.
- 7      Skipped Sequences    Sequence(s)            missing. If intentional, please insert the following lines for each skipped sequence (OLD RULES)
  - (2) INFORMATION FOR SEQ ID NO X (insert SEQ ID NO where "X" is shown)
  - (i) SEQUENCE CHARACTERISTICS (Do not insert any subheadings under this heading)
  - (xi) SEQUENCE DESCRIPTION SEQ ID NO X (insert SEQ ID NO where "X" is shown)
 This sequence is intentionally skipped  
  
 Please also adjust the "(ii) NUMBER OF SEQUENCES" response to include the skipped sequences
- 8      Skipped Sequences    Sequence(s)            missing. If intentional, please insert the following lines for each skipped sequence (NEW RULES)
  - <210> sequence id number
  - <400> sequence id number
  - 000
- 9      Use of n's or Xaa's    Use of n's and/or Xaa's have been detected in the Sequence Listing (NEW RULES)
  - Per 1.823 of Sequence Rules, use of <220>-<223> is MANDATORY if n's or Xaa's are present
  - In <220> to <223> section, please explain location of n or Xaa, and which residue n or Xaa represents
- 10      Invalid <213>    Per 1.823 of Sequence Rules, the only valid <213> responses are Unknown, Artificial Sequence, or Response    scientific name (Genus/species) <220>-<223> section is required when <213> response is Unknown or is Artificial Sequence
- 11      Use of <220>    Sequence(s) 45, 46, 50, 51, 63, 65, 83 missing the <220>-<223> section  
 Use of <220> to <223> is MANDATORY if <213> "Organism" response is "Artificial Sequence" or "Unknown." Please explain source of genetic material in <220> to <223> section.  
 (See "Federal Register," 00/01/1998, Vol. 63, No. 104, pp. 29631-32) (Sec. 1.823 of Sequence Rules)
- 12      PatentIn 2.0    Please do not use "Copy to Disk" function of PatentIn version 2.0. This causes a corrupted file, "bug"    resulting in missing mandatory numeric identifiers and responses (as indicated on raw sequence listing). Instead, please use "File Manager" or any other manual means to copy file to floppy disk.
- 13      Misuse of n/Xaa    "n" can only represent a single nucleotide; "Xaa" can only represent a single amino acid



IFWO

## RAW SEQUENCE LISTING

PATENT APPLICATION: US/10/714,781

DATE: 10/18/2004

TIME: 14:26:45

Input Set : A:\57431615.app

Output Set: N:\CRF4\10182004\J714781.raw

Does Not Comply  
Corrected Diskette Needed

(P5.1-4)

3 <110> APPLICANT: LOOSMORE, SHEENA MAY  
4 MINKE, JULES MAARTEN  
6 <120> TITLE OF INVENTION: RECOMBINANT VACCINE AGAINST WEST NILE VIRUS  
8 <130> FILE REFERENCE: 574313-3161.5  
10 <140> CURRENT APPLICATION NUMBER: 10/714,781  
11 <141> CURRENT FILING DATE: 2003-11-17  
13 <150> PRIOR APPLICATION NUMBER: 10/679,520  
14 <151> PRIOR FILING DATE: 2003-10-06  
16 <150> PRIOR APPLICATION NUMBER: 10/374,953  
17 <151> PRIOR FILING DATE: 2003-02-26  
19 <150> PRIOR APPLICATION NUMBER: 10/116,298  
20 <151> PRIOR FILING DATE: 2002-04-04  
22 <150> PRIOR APPLICATION NUMBER: 60/281,923  
23 <151> PRIOR FILING DATE: 2001-04-06  
25 <150> PRIOR APPLICATION NUMBER: 10/676,502  
26 <151> PRIOR FILING DATE: 2003-09-30  
28 <150> PRIOR APPLICATION NUMBER: PCT/FR02/01200  
29 <151> PRIOR FILING DATE: 2002-04-05  
31 <160> NUMBER OF SEQ ID NOS: 85  
33 <170> SOFTWARE: PatentIn Ver. 3.2

## ERRORED SEQUENCES

631 &lt;210&gt; SEQ ID NO: 45

632 &lt;211&gt; LENGTH: 10

633 &lt;212&gt; TYPE: PRT

634 &lt;213&gt; ORGANISM: Artificial Sequence

W--> 636 <220> FEATURE: peptide insert (220), whenever (221),  
636 <223> OTHER INFORMATION: Description of Artificial Sequence: Synthetic (222)  
637 peptide on (223) is present.

E--&gt; 639 &lt;400&gt; SEQUENCE: 45

640 Leu Leu Phe Leu Ser Val Asn Val His Ala

641 1 5 10

645 &lt;210&gt; SEQ ID NO: 46

646 &lt;211&gt; LENGTH: 8

647 &lt;212&gt; TYPE: PRT

648 &lt;213&gt; ORGANISM: Artificial Sequence

W--> 650 <220> FEATURE: peptide insert (220), whenever (221),  
650 <223> OTHER INFORMATION: Description of Artificial Sequence: Synthetic (222)  
651 peptide on (223) is present.

E--&gt; 653 &lt;400&gt; SEQUENCE: 46

654 Lys Pro Thr Ile Asp Val Lys Met

## RAW SEQUENCE LISTING

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Input Set : A:\57431615.app

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655 1 5

714 &lt;210&gt; SEQ ID NO: 50

715 &lt;211&gt; LENGTH: 8

716 &lt;212&gt; TYPE: PRT

717 &lt;213&gt; ORGANISM: Artificial Sequence

W--&gt; 719 &lt;220&gt; FEATURE:

719 &lt;223&gt; OTHER INFORMATION: Description of Artificial Sequence: Synthetic

720 peptide

OK 722 &lt;400&gt; SEQUENCE: 50

723 Lys Pro Thr Ile Asp Val Lys Met

724 1 5

728 &lt;210&gt; SEQ ID NO: 51

729 &lt;211&gt; LENGTH: 10

730 &lt;212&gt; TYPE: PRT

731 &lt;213&gt; ORGANISM: Artificial Sequence

W--&gt; 733 &lt;220&gt; FEATURE:

733 &lt;223&gt; OTHER INFORMATION: Description of Artificial Sequence: Synthetic

734 peptide

OK 736 &lt;400&gt; SEQUENCE: 51

737 Met Thr Gly Ile Ala Val Met Ile Gly Leu

738 1 5 10

2420 &lt;210&gt; SEQ ID NO: 63

2421 &lt;211&gt; LENGTH: 9

2422 &lt;212&gt; TYPE: PRT

2423 &lt;213&gt; ORGANISM: Artificial Sequence

W--&gt; 2425 &lt;220&gt; FEATURE:

2425 &lt;223&gt; OTHER INFORMATION: Description of Artificial Sequence: Synthetic

2426 peptide

OK 2428 &lt;400&gt; SEQUENCE: 63

2429 Thr Gly Ile Ala Val Met Ile Gly Leu

2430 1 5

2453 &lt;210&gt; SEQ ID NO: 65

2454 &lt;211&gt; LENGTH: 10

2455 &lt;212&gt; TYPE: PRT

2456 &lt;213&gt; ORGANISM: Artificial Sequence

W--&gt; 2458 &lt;220&gt; FEATURE:

2458 &lt;223&gt; OTHER INFORMATION: Description of Artificial Sequence: Synthetic

2459 peptide

OK 2461 &lt;400&gt; SEQUENCE: 65

2462 Met Thr Gly Ile Ala Val Met Ile Gly Leu

2463 1 5 10

4436 &lt;210&gt; SEQ ID NO: 83

4437 &lt;211&gt; LENGTH: 12

4438 &lt;212&gt; TYPE: PRT

4439 &lt;213&gt; ORGANISM: Artificial Sequence

W--&gt; 4441 &lt;220&gt; FEATURE:

4441 &lt;223&gt; OTHER INFORMATION: Description of Artificial Sequence: Synthetic VQH6

4442 amplified fragment

OK 4444 &lt;400&gt; SEQUENCE: 83

RAW SEQUENCE LISTING

PATENT APPLICATION: US/10/714,781

DATE: 10/18/2004

TIME: 14:26:46

Input Set : A:\57431615.app

Output Set: N:\CRF4\10182004\J714781.raw

4445	Val	Ile	Arg	Gln	Gly	Glu	Asn	Glu	Thr	Ile	Cys	Ser
4446	1				5					10		

## VERIFICATION SUMMARY

DATE: 10/18/2004

PATENT APPLICATION: US/10/714,781

TIME: 14:26:47

Input Set : A:\57431615.app

Output Set: N:\CRF4\10182004\J714781.raw

:636 M:258 W: Mandatory Feature missing, <220> Tag not found for SEQ ID#:45 ✓  
:639 M:200 E: Mandatory Header Field missing, <220> Tag not found for SEQ ID#:45 ✓  
:650 M:258 W: Mandatory Feature missing, <220> Tag not found for SEQ ID#:46 ✓  
:653 M:200 E: Mandatory Header Field missing, <220> Tag not found for SEQ ID#:46 ✓  
:719 M:258 W: Mandatory Feature missing, <220> Tag not found for SEQ ID#:50 ✓  
:722 M:200 E: Mandatory Header Field missing, <220> Tag not found for SEQ ID#:50 ✓  
:733 M:258 W: Mandatory Feature missing, <220> Tag not found for SEQ ID#:51 ✓  
:736 M:200 E: Mandatory Header Field missing, <220> Tag not found for SEQ ID#:51 ✓  
:2163 M:336 W: Invalid Amino Acid Number in Coding Region, SEQ ID:60  
:2425 M:258 W: Mandatory Feature missing, <220> Tag not found for SEQ ID#:63 ✓  
:2428 M:200 E: Mandatory Header Field missing, <220> Tag not found for SEQ ID#:63 ✓  
:2458 M:258 W: Mandatory Feature missing, <220> Tag not found for SEQ ID#:65 ✓  
:2461 M:200 E: Mandatory Header Field missing, <220> Tag not found for SEQ ID#:65 ✓  
:4441 M:258 W: Mandatory Feature missing, <220> Tag not found for SEQ ID#:83 ✓  
:4444 M:200 E: Mandatory Header Field missing, <220> Tag not found for SEQ ID#:83 ✓